



SEQUENCE LISTING

<110> Skeiky, Yasir
Guderian, Jeffrey
Corixa Corporation

<120> Methods of Using a Mycobacterium tuberculosis Coding
Sequence to Facilitate Stable and High Yield Expression
of Heterologous Proteins

<130> 014058-008010US

<140> US 09/684,215

<141> 2000-10-06

<150> US 60/158,585

<151> 1999-10-07

<160> 23

<170> PatentIn Ver. 2.1

<210> 1

<211> 1872

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> 32 KD serine protease MTB32A

<220>

<221> CDS

<222> (89)..(1156)

<223> MTB32A

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<222> (89)..(184)

<223> N-terminal hydrophobic secretory signal sequence

<220>

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<222> (185)..(1153)

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Met Ser Asn Ser Arg Arg Arg Ser
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ctc agg tgg tca tgg ttg ctg agc gtg ctg gct gcc gtc ggg ctg ggc 160
Leu Arg Trp Ser Trp Leu Leu Ser Val Leu Ala Ala Val Gly Leu Gly
-20 -15 -10

ctg gcc acg gcg ccg gcc cag gcg gcc ccg ccg gcc ttg tcg cag gac 208
Leu Ala Thr Ala Pro Ala Gln Ala Ala Pro Pro Ala Leu Ser Gln Asp
-5 -1 1 5

cgg ttc gcc gac ttc ccc gcg ctg ccc ctc gac ccg tcc gcg atg gtc	256
Arg Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val	
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gcc caa gtg ggg cca cag gtg gtc aac atc aac acc aaa ctg ggc tac	304
Ala Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr	
25 30 35 40	
aac aac gcc gtg ggc gcc ggg acc ggc atc gtc atc gat ccc aac ggt	352
Asn Asn Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly	
45 50 55	
gtc gtg ctg acc aac aac cac gtg atc gcg ggc gcc acc gac atc aat	400
Val Val Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn	
60 65 70	
gcg ttc agc gtc ggc tcc ggc caa acc tac ggc gtc gat gtg gtc ggg	448
Ala Phe Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly	
75 80 85	
tat gac cgc acc cag gat gtc gcg gtg ctg cag ctg cgc ggt gcc ggt	496
Tyr Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly	
90 95 100	
ggc ctg ccg tcc gcg gcg atc ggt ggc ggc gtc gcg gtt ggt gag ccc	544
Gly Leu Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro	
105 110 115 120	
gtc gtc gcg atg ggc aac agc ggt ggg cag ggc gga acg ccc cgt gcg	592
Val Val Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala	
125 130 135	
gtg cct ggc agg gtg gtc gcg ctc ggc caa acc gtg cag gcg tcc gat	640
Val Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp	
140 145 150	
tcg ctg acc ggt gcc gaa gag aca ttg aac ggg ttg atc cag ttc gat	688
Ser Leu Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp	
155 160 165	
gcc gcg atc cag ccc ggt gat tcg ggc ggg ccc gtc gtc aac ggc cta	736
Ala Ala Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu	
170 175 180	
gga cag gtg gtc ggt atg aac acg gcc gcg tcc gat aac ttc cag ctg	784
Gly Gln Val Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu	
185 190 195 200	
tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg gcg	832
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala	
205 210 215	
atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat atc	880
Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile	
220 225 230	
ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc aac	928
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn	
235 240 245	

ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt ctc 976
 Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
 250 255 260

ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg atc 1024
 Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
 265 270 275 280

aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc ggt 1072
 Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
 285 290 295

gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt aca 1120
 Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
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ggg aac gtg aca ttg gcc gag gga ccc ccg gcc tga tttcgctcgcg 1166
 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
 315 320

gataccacccc gccggccggc caattggatt ggcgccagcc gtgattgccg cgtgagcccc 1226
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 <213> Mycobacterium tuberculosis

<220>
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 35 40 45

Pro	Leu	Asp	Pro	Ser	Ala	Met	Val	Ala	Gln	Val	Gly	Pro	Gln	Val	Val
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65					70					75					80
Gly	Ile	Val	Ile	Asp	Pro	Asn	Gly	Val	Val	Leu	Thr	Asn	Asn	His	Val
				85						90				95	
Ile	Ala	Gly	Ala	Thr	Asp	Ile	Asn	Ala	Phe	Ser	Val	Gly	Ser	Gly	Gln
			100					105					110		
Thr	Tyr	Gly	Val	Asp	Val	Val	Gly	Tyr	Asp	Arg	Thr	Gln	Asp	Val	Ala
		115					120					125			
Val	Leu	Gln	Leu	Arg	Gly	Ala	Gly	Gly	Leu	Pro	Ser	Ala	Ala	Ile	Gly
	130					135					140				
Gly	Gly	Val	Ala	Val	Gly	Glu	Pro	Val	Val	Ala	Met	Gly	Asn	Ser	Gly
145					150					155					160
Gly	Gln	Gly	Gly	Thr	Pro	Arg	Ala	Val	Pro	Gly	Arg	Val	Val	Ala	Leu
				165					170					175	
Gly	Gln	Thr	Val	Gln	Ala	Ser	Asp	Ser	Leu	Thr	Gly	Ala	Glu	Glu	Thr
			180					185					190		
Leu	Asn	Gly	Leu	Ile	Gln	Phe	Asp	Ala	Ala	Ile	Gln	Pro	Gly	Asp	Ser
	195					200						205			
Gly	Gly	Pro	Val	Val	Asn	Gly	Leu	Gly	Gln	Val	Val	Gly	Met	Asn	Thr
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Ala	Ala	Ser	Asp	Asn	Phe	Gln	Leu	Ser	Gln	Gly	Gly	Gln	Gly	Phe	Ala
225					230					235					240
Ile	Pro	Ile	Gly	Gln	Ala	Met	Ala	Ile	Ala	Gly	Gln	Ile	Arg	Ser	Gly
			245						250					255	
Gly	Gly	Ser	Pro	Thr	Val	His	Ile	Gly	Pro	Thr	Ala	Phe	Leu	Gly	Leu
			260					265					270		
Gly	Val	Val	Asp	Asn	Asn	Gly	Asn	Gly	Ala	Arg	Val	Gln	Arg	Val	Val
	275						280					285			
Gly	Ser	Ala	Pro	Ala	Ala	Ser	Leu	Gly	Ile	Ser	Thr	Gly	Asp	Val	Ile
	290					295					300				
Thr	Ala	Val	Asp	Gly	Ala	Pro	Ile	Asn	Ser	Ala	Thr	Ala	Met	Ala	Asp
305					310					315					320
Ala	Leu	Asn	Gly	His	His	Pro	Gly	Asp	Val	Ile	Ser	Val	Thr	Trp	Gln
			325						330					335	
Thr	Lys	Ser	Gly	Gly	Thr	Arg	Thr	Gly	Asn	Val	Thr	Leu	Ala	Glu	Gly
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Pro	Pro	Ala													
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<210> 3

<211> 396

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> 14 KD C-terminal fragment of MTB32A Ra12

<220>

<221> CDS

<222> (1) .. (396)

<223> Ra12

<400> 3

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1					5				10					15		

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gcc att ccg atc ggg cag gcg atg gcg atc gcg ggc cag atc cga tcg   96
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
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ggg ggg ggg tca ccc acc gtt cat atc ggg cct acc gcc ttc ctc ggc   144
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
      35                      40                      45

ttg ggt gtt gtc gac aac aac ggc aac ggc gca cga gtc caa cgc gtg   192
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
      50                      55                      60

gtc ggg agc gct ccg gcg gca agt ctc ggc atc tcc acc ggc gac gtg   240
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
      65                      70                      75                      80

atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc acc gcg atg gcg   288
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
      85                      90                      95

gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg acc tgg   336
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
      100                     105                     110

caa acc aag tcg ggc ggc acg cgt aca ggg aac gtg aca ttg gcc gag   384
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
      115                     120                     125

gga ccc ccg gcc
Gly Pro Pro Ala
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 <213> Mycobacterium tuberculosis

<220>
 <223> 14 KD C-terminal fragment of MTB32A Ra12

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      20      25      30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
      35      40      45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
      50      55      60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
      65      70      75      80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
      85      90      95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
      100     105     110
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Gly Pro Pro Ala
      130

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<210> 5
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 <213> Artificial Sequence

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<220>
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 <223> Ral2-DPPD fusion polypeptide

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ctg tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg 96
Leu Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met
          20          25          30

gcg atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat 144
Ala Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His
          35          40          45

atc ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc 192
Ile Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly
    50          55          60

aac ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt 240
Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser
    65          70          75

ctc ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg 288
Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro
    80          85          90          95

atc aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc 336
Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro
          100          105          110

ggt gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt 384
Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg
          115          120          125

aca ggg aac gtg aca ttg gcc gag gga ccc ccg gcc gaa ttc gac gac 432
Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Asp Asp
          130          135          140

gac gac aag gat cca cct gac ccg cat cag ccg gac atg acg aaa ggc 480
Asp Asp Lys Asp Pro Pro Asp Pro His Gln Pro Asp Met Thr Lys Gly
          145          150          155

tat tgc ccg ggt ggc cga tgg ggt ttt ggc gac ttg gcc gtg tgc gac 528
Tyr Cys Pro Gly Gly Arg Trp Gly Phe Gly Asp Leu Ala Val Cys Asp
          160          165          170          175

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ggc gag aag tac ccc gac ggc tcg ttt tgg cac cag tgg atg caa acg 576
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180 185 190

tgg ttt acc ggc cca cag ttt tac ttc gat tgt gtc agc ggc ggt gag 624
Trp Phe Thr Gly Pro Gln Phe Tyr Phe Asp Cys Val Ser Gly Gly Glu
195 200 205

ccc ctc ccc ggc ccg ccg cca ccg ggt ggt tgc ggt ggg gca att ccg 672
Pro Leu Pro Gly Pro Pro Pro Pro Gly Gly Cys Gly Gly Ala Ile Pro
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Ser Glu Gln Pro Asn Ala Pro
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<210> 6
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<212> PRT
<213> Artificial Sequence

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<220>
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Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
          35          40          45
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
          50          55          60
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
          65          70          75          80
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
          85          90          95
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
          100          105          110
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
          115          120          125
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Asp Asp Asp
          130          135          140
Asp Lys Asp Pro Pro Asp Pro His Gln Pro Asp Met Thr Lys Gly Tyr
          145          150          155          160
Cys Pro Gly Gly Arg Trp Gly Phe Gly Asp Leu Ala Val Cys Asp Gly
          165          170          175
Glu Lys Tyr Pro Asp Gly Ser Phe Trp His Gln Trp Met Gln Thr Trp
          180          185          190
Phe Thr Gly Pro Gln Phe Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro
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Leu Pro Gly Pro Pro Pro Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser
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Glu Gln Pro Asn Ala Pro
          225          230

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 <212> DNA
 <213> Artificial Sequence

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 <222> (4)..(1740)
 <223> Ra12-WT1 fusion polypeptide

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 Leu Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met
 20 25 30
 gcg atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat 144
 Ala Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His
 35 40 45
 atc ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc 192
 Ile Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly
 50 55 60
 aac ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt 240
 Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser
 65 70 75
 ctc ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg 288
 Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro
 80 85 90 95
 atc aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc 336
 Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro
 100 105 110
 ggt gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt 384
 Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg
 115 120 125
 aca ggg aac gtg aca ttg gcc gag gga ccc ccg gcc gaa ttc ccg ctg 432
 Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Pro Leu
 130 135 140
 gtg ccg cgc ggc agc ccg atg ggc tcc gac gtt cgg gac ctg aac gca 480
 Val Pro Arg Gly Ser Pro Met Gly Ser Asp Val Arg Asp Leu Asn Ala
 145 150 155
 ctg ctg ccg gca gtt ccg tcc ctg ggt ggt ggt ggt ggt tgc gca ctg 528
 Leu Leu Pro Ala Val Pro Ser Leu Gly Gly Gly Gly Gly Cys Ala Leu
 160 165 170 175
 ccg gtt agc ggt gca gca cag tgg gct ccg gtt ctg gac ttc gca ccg 576
 Pro Val Ser Gly Ala Ala Gln Trp Ala Pro Val Leu Asp Phe Ala Pro
 180 185 190

ccg ggt gca tcc gca tac ggt tcc ctg ggt ggt ccg gca ccg ccg ccg Pro Gly Ala Ser Ala Tyr Gly Ser Leu Gly Gly Pro Ala Pro Pro Pro	624
195 200 205	
gca ccg ccg ccg ccg ccg ccg ccg ccg ccg ccg cac tcc ttc atc aaa cag Ala Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro His Ser Phe Ile Lys Gln	672
210 215 220	
gaa ccg agc tgg ggt ggt gca gaa ccg cac gaa gaa cag tgc ctg agc Glu Pro Ser Trp Gly Gly Ala Glu Pro His Glu Glu Cys Leu Ser	720
225 230 235	
gca ttc acc gtt cac ttc tcc ggc cag ttc act ggc aca gcc gga gcc Ala Phe Thr Val His Phe Ser Gly Gln Phe Thr Gly Thr Ala Gly Ala	768
240 245 250 255	
tgt cgc tac ggg ccc ttc ggt cct cct ccg ccc agc cag gcg tca tcc Cys Arg Tyr Gly Pro Phe Gly Pro Pro Pro Pro Ser Gln Ala Ser Ser	816
260 265 270	
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275 280 285	
gag agc cag ccc gct att cgc aat cag ggt tac agc acg gtc acc ttc Glu Ser Gln Pro Ala Ile Arg Asn Gln Gly Tyr Ser Thr Val Thr Phe	912
290 295 300	
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305 310 315	
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340 345 350	
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355 360 365	
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370 375 380	
tgc atg acc tgg aat cag atg aac tta gga gcc acc tta aag ggc cac Cys Met Thr Trp Asn Gln Met Asn Leu Gly Ala Thr Leu Lys Gly His	1200
385 390 395	
agc aca ggg tac gag agc gat aac cac aca acg ccc atc ctc tgc gga Ser Thr Gly Tyr Glu Ser Asp Asn His Thr Thr Pro Ile Leu Cys Gly	1248
400 405 410 415	
gcc caa tac aga ata cac acg cac ggt gtc ttc aga ggc att cag gat Ala Gln Tyr Arg Ile His Thr His Gly Val Phe Arg Gly Ile Gln Asp	1296
420 425 430	

gtg cga cgt gtg cct gga gta gcc ccg act ctt gta cgg tcg gca tct	1344
Val Arg Arg Val Pro Gly Val Ala Pro Thr Leu Val Arg Ser Ala Ser	
435 440 445	
gag acc agt gag aaa cgc ccc ttc atg tgt gct tac tca ggc tgc aat	1392
Glu Thr Ser Glu Lys Arg Pro Phe Met Cys Ala Tyr Ser Gly Cys Asn	
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aag aga tat ttt aag ctg tcc cac tta cag atg cac agc agg aag cac	1440
Lys Arg Tyr Phe Lys Leu Ser His Leu Gln Met His Ser Arg Lys His	
465 470 475	
act ggt gag aaa cca tac cag tgt gac ttc aag gac tgt gaa cga agg	1488
Thr Gly Glu Lys Pro Tyr Gln Cys Asp Phe Lys Asp Cys Glu Arg Arg	
480 485 490 495	
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Phe Phe Arg Ser Asp Gln Leu Lys Arg His Gln Arg Arg His Thr Gly	
500 505 510	
gtg aaa cca ttc cag tgt aaa act tgt cag cga aag ttc tcc cgg tcc	1584
Val Lys Pro Phe Gln Cys Lys Thr Cys Gln Arg Lys Phe Ser Arg Ser	
515 520 525	
gac cac ctg aag acc cac acc agg act cat aca ggt gaa aag ccc ttc	1632
Asp His Leu Lys Thr His Thr Arg Thr His Thr Gly Glu Lys Pro Phe	
530 535 540	
agc tgt cgg tgg cca agt tgt cag aaa aag ttt gcc cgg tca gat gaa	1680
Ser Cys Arg Trp Pro Ser Cys Gln Lys Lys Phe Ala Arg Ser Asp Glu	
545 550 555	
tta gtc cgc cat cac aac atg cat cag aga aac atg acc aaa ctc cag	1728
Leu Val Arg His His Asn Met His Gln Arg Asn Met Thr Lys Leu Gln	
560 565 570 575	
ctg gcg ctt tga gaattc	1746
Leu Ala Leu	

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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ral2-WT1 fusion polypeptide

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Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu	
1 5 10 15	
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala	
20 25 30	
Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile	
35 40 45	
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn	
50 55 60	
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu	
65 70 75 80	

Gly	Ile	Ser	Thr	Gly	Asp	Val	Ile	Thr	Ala	Val	Asp	Gly	Ala	Pro	Ile	
				85					90					95		
Asn	Ser	Ala	Thr	Ala	Met	Ala	Asp	Ala	Leu	Asn	Gly	His	His	Pro	Gly	
			100					105					110			
Asp	Val	Ile	Ser	Val	Thr	Trp	Gln	Thr	Lys	Ser	Gly	Gly	Thr	Arg	Thr	
		115					120					125				
Gly	Asn	Val	Thr	Leu	Ala	Glu	Gly	Pro	Pro	Ala	Glu	Phe	Pro	Leu	Val	
	130					135					140					
Pro	Arg	Gly	Ser	Pro	Met	Gly	Ser	Asp	Val	Arg	Asp	Leu	Asn	Ala	Leu	
145					150					155					160	
Leu	Pro	Ala	Val	Pro	Ser	Leu	Gly	Gly	Gly	Gly	Gly	Cys	Ala	Leu	Pro	
				165					170					175		
Val	Ser	Gly	Ala	Ala	Gln	Trp	Ala	Pro	Val	Leu	Asp	Phe	Ala	Pro	Pro	
			180				185						190			
Gly	Ala	Ser	Ala	Tyr	Gly	Ser	Leu	Gly	Gly	Pro	Ala	Pro	Pro	Pro	Ala	
		195					200					205				
Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	His	Ser	Phe	Ile	Lys	Gln	Glu	
	210					215					220					
Pro	Ser	Trp	Gly	Gly	Ala	Glu	Pro	His	Glu	Glu	Gln	Cys	Leu	Ser	Ala	
225					230					235					240	
Phe	Thr	Val	His	Phe	Ser	Gly	Gln	Phe	Thr	Gly	Thr	Ala	Gly	Ala	Cys	
				245				250						255		
Arg	Tyr	Gly	Pro	Phe	Gly	Pro	Pro	Pro	Pro	Ser	Gln	Ala	Ser	Ser	Gly	
			260				265						270			
Gln	Ala	Arg	Met	Phe	Pro	Asn	Ala	Pro	Tyr	Leu	Pro	Ser	Cys	Leu	Glu	
		275					280					285				
Ser	Gln	Pro	Ala	Ile	Arg	Asn	Gln	Gly	Tyr	Ser	Thr	Val	Thr	Phe	Asp	
	290					295					300					
Gly	Thr	Pro	Ser	Tyr	Gly	His	Thr	Pro	Ser	His	His	Ala	Ala	Gln	Phe	
305					310					315					320	
Pro	Asn	His	Ser	Phe	Lys	His	Glu	Asp	Pro	Met	Gly	Gln	Gln	Gly	Ser	
				325				330						335		
Leu	Gly	Glu	Gln	Gln	Tyr	Ser	Val	Pro	Pro	Pro	Val	Tyr	Gly	Cys	His	
			340				345					350				
Thr	Pro	Thr	Asp	Ser	Cys	Thr	Gly	Ser	Gln	Ala	Leu	Leu	Leu	Arg	Thr	
		355					360					365				
Pro	Tyr	Ser	Ser	Asp	Asn	Leu	Tyr	Gln	Met	Thr	Ser	Gln	Leu	Glu	Cys	
	370					375					380					
Met	Thr	Trp	Asn	Gln	Met	Asn	Leu	Gly	Ala	Thr	Leu	Lys	Gly	His	Ser	
385					390					395					400	
Thr	Gly	Tyr	Glu	Ser	Asp	Asn	His	Thr	Thr	Pro	Ile	Leu	Cys	Gly	Ala	
				405				410						415		
Gln	Tyr	Arg	Ile	His	Thr	His	Gly	Val	Phe	Arg	Gly	Ile	Gln	Asp	Val	
			420				425						430			
Arg	Arg	Val	Pro	Gly	Val	Ala	Pro	Thr	Leu	Val	Arg	Ser	Ala	Ser	Glu	
		435					440					445				
Thr	Ser	Glu	Lys	Arg	Pro	Phe	Met	Cys	Ala	Tyr	Ser	Gly	Cys	Asn	Lys	
	450					455					460					
Arg	Tyr	Phe	Lys	Leu	Ser	His	Leu	Gln	Met	His	Ser	Arg	Lys	His	Thr	
465					470					475					480	
Gly	Glu	Lys	Pro	Tyr	Gln	Cys	Asp	Phe	Lys	Asp	Cys	Glu	Arg	Arg	Phe	
				485				490						495		
Phe	Arg	Ser	Asp	Gln	Leu	Lys	Arg	His	Gln	Arg	Arg	His	Thr	Gly	Val	
			500					505					510			
Lys	Pro	Phe	Gln	Cys	Lys	Thr	Cys	Gln	Arg	Lys	Phe	Ser	Arg	Ser	Asp	
		515					520					525				
His	Leu	Lys	Thr	His	Thr	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Phe	Ser	
	530					535					540					
Cys	Arg	Trp	Pro	Ser	Cys	Gln	Lys	Lys	Phe	Ala	Arg	Ser	Asp	Glu	Leu	
545					550					555					560	

Val Arg His His Asn Met His Gln Arg Asn Met Thr Lys Leu Gln Leu
565 570 575
Ala Leu

<210> 9
<211> 672
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ra12-human mammaglobin fusion

<220>
<221> CDS
<222> (4)..(666)
<223> Ra12-human mammaglobin fusion polypeptide

<400> 9
cat atg cat cac cat cac cat cac acg gcc gcg tcc gat aac ttc cag 48
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln
1 5 10 15
ctg tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg 96
Leu Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met
20 25 30
gcg atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat 144
Ala Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His
35 40 45
atc ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc 192
Ile Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly
50 55 60
aac ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt 240
Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser
65 70 75
ctc ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg 288
Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro
80 85 90 95
atc aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc 336
Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro
100 105 110
ggt gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt 384
Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg
115 120 125
aca ggg aac gtg aca ttg gcc gag gga ccc ccg gcc gaa ttc atc gag 432
Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Ile Glu
130 135 140
gga agg ggc tct ggc tgc ccc tta ttg gag aat gtg att tcc aag aca 480
Gly Arg Gly Ser Gly Cys Pro Leu Leu Glu Asn Val Ile Ser Lys Thr
145 150 155

atc aat cca caa gtg tct aag act gaa tac aaa gaa ctt ctt caa gag	528
Ile Asn Pro Gln Val Ser Lys Thr Glu Tyr Lys Glu Leu Leu Gln Glu	
160 165 170 175	
ttc ata gac gac aat gcc act aca aat gcc ata gat gaa ttg aag gaa	576
Phe Ile Asp Asp Asn Ala Thr Thr Asn Ala Ile Asp Glu Leu Lys Glu	
180 185 190	
tgt ttt ctt aac caa acg gat gaa act ctg agc aat gtt gag gtg ttt	624
Cys Phe Leu Asn Gln Thr Asp Glu Thr Leu Ser Asn Val Glu Val Phe	
195 200 205	
atg caa tta ata tat gac agc agt ctt tgt gat tta ttt taa gaattc	672
Met Gln Leu Ile Tyr Asp Ser Ser Leu Cys Asp Leu Phe	
210 215 220	

<210> 10

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ra12-human mammaglobin fusion polypeptide

<400> 10

Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu	
1 5 10 15	
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala	
20 25 30	
Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile	
35 40 45	
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn	
50 55 60	
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu	
65 70 75 80	
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile	
85 90 95	
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly	
100 105 110	
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr	
115 120 125	
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Ile Glu Gly	
130 135 140	
Arg Gly Ser Gly Cys Pro Leu Leu Glu Asn Val Ile Ser Lys Thr Ile	
145 150 155 160	
Asn Pro Gln Val Ser Lys Thr Glu Tyr Lys Glu Leu Leu Gln Glu Phe	
165 170 175	
Ile Asp Asp Asn Ala Thr Thr Asn Ala Ile Asp Glu Leu Lys Glu Cys	
180 185 190	
Phe Leu Asn Gln Thr Asp Glu Thr Leu Ser Asn Val Glu Val Phe Met	
195 200 205	
Gln Leu Ile Tyr Asp Ser Ser Leu Cys Asp Leu Phe	
210 215 220	

<210> 11

<211> 2191

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ra12-H9-32A fusion
(Ra12-MTB39-MTB32A(N-ter) fusion)

<220>

<221> CDS

<222> (1)..(2190)

<223> Ra12-H9-32A (Ra12-MTB39-MTB32A(N-ter)) fusion polypeptide

<400> 11

atg cat cac cat cac cat cac acg gcc gcg tcc gat aac ttc cag ctg	48
Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu	
1 5 10 15	
tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg gcg	96
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala	
20 25 30	
atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat atc	144
Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile	
35 40 45	
ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc aac	192
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn	
50 55 60	
ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt ctc	240
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu	
65 70 75 80	
ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg atc	288
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile	
85 90 95	
aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc ggt	336
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly	
100 105 110	
gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt aca	384
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr	
115 120 125	
ggg aac gtg aca ttg gcc gag gga ccc ccg gcc gaa ttc atg gtg gat	432
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp	
130 135 140	
ttc ggg gcg tta cca ccg gag atc aac tcc gcg agg atg tac gcc ggc	480
Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly	
145 150 155 160	
ccg ggt tcg gcc tcg ctg gtg gcc gcg gct cag atg tgg gac agc gtg	528
Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val	
165 170 175	
gcg agt gac ctg ttt tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg	576
Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp	
180 185 190	
ggt ctg acg gtg ggg tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg	624
Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val	
195 200 205	

gcg gcg gcc tcg ccg tat gtg gcg tgg atg agc gtc acc gcg ggg cag Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln 210 215 220	672
gcc gag ctg acc gcc gcc cag gtc cgg gtt gct gcg gcg gcc tac gag Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Tyr Glu 225 230 235 240	720
acg gcg tat ggg ctg acg gtg ccc ccg ccg gtg atc gcc gag aac cgt Thr Ala Tyr Gly Leu Thr Val Pro Pro Val Ile Ala Glu Asn Arg 245 250 255	768
gct gaa ctg atg att ctg ata gcg acc aac ctc ttg ggg caa aac acc Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr 260 265 270	816
ccg gcg atc gcg gtc aac gag gcc gaa tac ggc gag atg tgg gcc caa Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln 275 280 285	864
gac gcc gcc gcg atg ttt ggc tac gcc gcg gcg acg gcg acg gcg acg Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr 290 295 300	912
gcg acg ttg ctg ccg ttc gag gag gcg ccg gag atg acc agc gcg ggt Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly 305 310 315 320	960
ggg ctc ctc gag cag gcc gcc gcg gtc gag gag gcc tcc gac acc gcc Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala 325 330 335	1008
gcg gcg aac cag ttg atg aac aat gtg ccc cag gcg ctg caa cag ctg Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu 340 345 350	1056
gcc cag ccc acg cag ggc acc acg cct tct tcc aag ctg ggt ggc ctg Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu 355 360 365	1104
tgg aag acg gtc tcg ccg cat cgg tcg ccg atc agc aac atg gtg tcg Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser 370 375 380	1152
atg gcc aac aac cac atg tcg atg acc aac tcg ggt gtg tcg atg acc Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr 385 390 395 400	1200
aac acc ttg agc tcg atg ttg aag ggc ttt gct ccg gcg gcg gcc gcc Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala 405 410 415	1248
cag gcc gtg caa acc gcg gcg caa aac ggg gtc cgg gcg atg agc tcg Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser 420 425 430	1296
ctg ggc agc tcg ctg ggt tct tcg ggt ctg ggc ggt ggg gtg gcc gcc Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala 435 440 445	1344

aac ttg ggt cgg gcg gcc tcg gtc ggt tcg ttg tcg gtg ccg cag gcc Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala 450 455 460	1392
tgg gcc gcg gcc aac cag gca gtc acc ccg gcg gcg cgg gcg ctg ccg Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro 465 470 475 480	1440
ctg acc agc ctg acc agc gcc gcg gaa aga ggg ccc ggg cag atg ctg Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu 485 490 495	1488
ggc ggg ctg ccg gtg ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu 500 505 510	1536
agt ggt gtg ctg cgt gtt ccg ccg cga ccc tat gtg atg ccg cat tct Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser 515 520 525	1584
ccg gca gcc ggc gat atc gcc ccg ccg gcc ttg tcg cag gac cgg ttc Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe 530 535 540	1632
gcc gac ttc ccc gcg ctg ccc ctc gac ccg tcc gcg atg gtc gcc caa Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln 545 550 555 560	1680
gtg ggg cca cag gtg gtc aac atc aac acc aaa ctg ggc tac aac aac Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn 565 570 575	1728
gcc gtg ggc gcc ggg acc ggc atc gtc atc gat ccc aac ggt gtc gtg Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val 580 585 590	1776
ctg acc aac aac cac gtg atc gcg ggc gcc acc gac atc aat gcg ttc Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe 595 600 605	1824
agc gtc ggc tcc ggc caa acc tac ggc gtc gat gtg gtc ggg tat gac Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp 610 615 620	1872
cgc acc cag gat gtc gcg gtg ctg cag ctg cgc ggt gcc ggt ggc ctg Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu 625 630 635 640	1920
ccg tcg gcg gcg atc ggt ggc ggc gtc gcg gtt ggt gag ccc gtc gtc Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val Val 645 650 655	1968
gcg atg ggc aac agc ggt ggg cag ggc gga acg ccc cgt gcg gtg cct Ala Met Gly Asn Ser Gly Gly Gln Gly Thr Pro Arg Ala Val Pro 660 665 670	2016
ggc agg gtg gtc gcg ctc ggc caa acc gtg cag gcg tcg gat tcg ctg Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu 675 680 685	2064

acc ggt gcc gaa gag aca ttg aac ggg ttg atc cag ttc gat gcc gcg 2112
 Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
 690 695 700

atc cag ccc ggt gat tcg ggc ggg ccc gtc gtc aac ggc cta gga cag 2160
 Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln
 705 710 715 720

gtg gtc ggt atg aac acg gcc gcg tcc tag g 2191
 Val Val Gly Met Asn Thr Ala Ala Ser
 725 730

<210> 12

<211> 729

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ral2-H9-32A fusion
 polypeptide (Ral2-MTB39-MTB32A(N-ter) fusion polypeptide)

<400> 12

Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
 1 5 10 15
 Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
 20 25 30
 Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile
 35 40 45
 Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
 50 55 60
 Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
 65 70 75 80
 Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
 85 90 95
 Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
 100 105 110
 Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
 115 120 125
 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp
 130 135 140
 Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly
 145 150 155 160
 Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val
 165 170 175
 Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp
 180 185 190
 Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val
 195 200 205
 Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln
 210 215 220
 Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Tyr Glu
 225 230 235 240
 Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg
 245 250 255
 Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr
 260 265 270
 Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln
 275 280 285
 Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Thr
 290 295 300

Ala	Thr	Leu	Leu	Pro	Phe	Glu	Glu	Ala	Pro	Glu	Met	Thr	Ser	Ala	Gly	305	310	315	320
Gly	Leu	Leu	Glu	Gln	Ala	Ala	Ala	Val	Glu	Glu	Ala	Ser	Asp	Thr	Ala	325	330		335
Ala	Ala	Asn	Gln	Leu	Met	Asn	Asn	Val	Pro	Gln	Ala	Leu	Gln	Gln	Leu	340	345		350
Ala	Gln	Pro	Thr	Gln	Gly	Thr	Thr	Pro	Ser	Ser	Lys	Leu	Gly	Gly	Leu	355	360		365
Trp	Lys	Thr	Val	Ser	Pro	His	Arg	Ser	Pro	Ile	Ser	Asn	Met	Val	Ser	370	375	380	
Met	Ala	Asn	Asn	His	Met	Ser	Met	Thr	Asn	Ser	Gly	Val	Ser	Met	Thr	385	390	395	400
Asn	Thr	Leu	Ser	Ser	Met	Leu	Lys	Gly	Phe	Ala	Pro	Ala	Ala	Ala	Ala	405	410		415
Gln	Ala	Val	Gln	Thr	Ala	Ala	Gln	Asn	Gly	Val	Arg	Ala	Met	Ser	Ser	420	425		430
Leu	Gly	Ser	Ser	Leu	Gly	Ser	Ser	Gly	Leu	Gly	Gly	Gly	Val	Ala	Ala	435	440	445	
Asn	Leu	Gly	Arg	Ala	Ala	Ser	Val	Gly	Ser	Leu	Ser	Val	Pro	Gln	Ala	450	455	460	
Trp	Ala	Ala	Ala	Asn	Gln	Ala	Val	Thr	Pro	Ala	Ala	Arg	Ala	Leu	Pro	465	470	475	480
Leu	Thr	Ser	Leu	Thr	Ser	Ala	Ala	Glu	Arg	Gly	Pro	Gly	Gln	Met	Leu	485	490		495
Gly	Gly	Leu	Pro	Val	Gly	Gln	Met	Gly	Ala	Arg	Ala	Gly	Gly	Gly	Leu	500	505		510
Ser	Gly	Val	Leu	Arg	Val	Pro	Pro	Arg	Pro	Tyr	Val	Met	Pro	His	Ser	515	520	525	
Pro	Ala	Ala	Gly	Asp	Ile	Ala	Pro	Pro	Ala	Leu	Ser	Gln	Asp	Arg	Phe	530	535	540	
Ala	Asp	Phe	Pro	Ala	Leu	Pro	Leu	Asp	Pro	Ser	Ala	Met	Val	Ala	Gln	545	550	555	560
Val	Gly	Pro	Gln	Val	Val	Asn	Ile	Asn	Thr	Lys	Leu	Gly	Tyr	Asn	Asn	565	570		575
Ala	Val	Gly	Ala	Gly	Thr	Gly	Ile	Val	Ile	Asp	Pro	Asn	Gly	Val	Val	580	585		590
Leu	Thr	Asn	Asn	His	Val	Ile	Ala	Gly	Ala	Thr	Asp	Ile	Asn	Ala	Phe	595	600	605	
Ser	Val	Gly	Ser	Gly	Gln	Thr	Tyr	Gly	Val	Asp	Val	Val	Gly	Tyr	Asp	610	615	620	
Arg	Thr	Gln	Asp	Val	Ala	Val	Leu	Gln	Leu	Arg	Gly	Ala	Gly	Gly	Leu	625	630	635	640
Pro	Ser	Ala	Ala	Ile	Gly	Gly	Gly	Val	Ala	Val	Gly	Glu	Pro	Val	Val	645	650		655
Ala	Met	Gly	Asn	Ser	Gly	Gly	Gln	Gly	Gly	Thr	Pro	Arg	Ala	Val	Pro	660	665	670	
Gly	Arg	Val	Val	Ala	Leu	Gly	Gln	Thr	Val	Gln	Ala	Ser	Asp	Ser	Leu	675	680	685	
Thr	Gly	Ala	Glu	Glu	Thr	Leu	Asn	Gly	Leu	Ile	Gln	Phe	Asp	Ala	Ala	690	695	700	
Ile	Gln	Pro	Gly	Asp	Ser	Gly	Gly	Pro	Val	Val	Asn	Gly	Leu	Gly	Gln	705	710	715	720
Val	Val	Gly	Met	Asn	Thr	Ala	Ala	Ser								725			

<210> 13

<211> 51

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide primer for PCR amplification of Ra12 C-terminal fragment of MTB32A

<400> 13
 caattacata tgcatacaca tcaccatcac acggccgcgt ccgataactt c 51

<210> 14
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:3' oligonucleotide primer for PCR amplification of Ra12 C-terminal fragment of MTB32A

<400> 14
 ctaatcgaat tcggccgggg gtccctcggc caa 33

<210> 15
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:5' oligonucleotide primer containing enterokinase recognition site for PCR amplification of DPPD mature secreted form

<400> 15
 caattagaat tcgacgacga cgacaaggat ccacctgacc cgcatacag 48

<210> 16
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:3' oligonucleotide primer containing enterokinase recognition site for PCR amplification of DPPD mature secreted form

<400> 16
 caattagaat tctcagggag cgttgggctg etc 33

<210> 17
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ra12(short) polypeptide

<400> 17
 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile
 20 25 30

<210> 18
 <211> 128
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ra12(long)
 polypeptide

<400> 18
 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Lys Leu
 20 25 30
 Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val
 35 40 45
 Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala
 50 55 60
 Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val
 65 70 75 80
 Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn
 85 90 95
 Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser
 100 105 110
 Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
 115 120 125

<210> 19
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:5'
 oligonucleotide primer, HindIII site, for PCR
 amplification of human mammaglobin

<400> 19
 gcgaagctta tgaagttgct gatggtcctc atgc

34

<210> 20
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:3'
 oligonucleotide primer, XhoI site, for PCR
 amplification of human mammaglobin

<400> 20
 cggctcgagt taaaataaat cacaaagact gctgtc

36

<210> 21
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Met-His tag 6aa

<400> 21
 Met His His His His His His
 1 5

<210> 22
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:enterokinase
 recognition site

<400> 22
 Asp Asp Asp Lys
 1

<210> 23
 <211> 128
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> positions 1-128 of Ra12

<400> 23
 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
 20 25 30
 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
 35 40 45
 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
 50 55 60
 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
 65 70 75 80
 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
 85 90 95
 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
 100 105 110
 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
 115 120 125